

Appendix B

NCBI

Entrez

BLAST 2 sequences

BLAST

Example

Help

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment.

The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program ☒ blastp ☒ Matrix ☐ Not ApplicableParameters used in BLASTN program only:Reward for a match: Penalty for a mismatch: ☐ Use Mega BLAST Strand option ☐ Both strands ☒Open gap and extension gap penalties
gap x_dropoff expect word size Filter ☒ Align Sequence 1 Enter accession or GI or download from file
or sequence in FASTA format from: to:

LXXXXXXXXXXEVLKKEQALQTVCL

Sequence 2 Enter accession or GI or download from file
or sequence in FASTA format from: to:

VASLRQQVEALQGQVQHLQAAFSQYKK

Align

Clear Input

Comments and suggestions to blast-help@ncbi.nlm.nih.gov

**Blast 2 Sequences results**

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]Matrix **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0000** wordsize: **3** Filter ☒ Align

Sequence 1 lc|seq_1 Length 26

Sequence 2 lc|seq_2 Length 27

No significant similarity was found

NCBI

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BLAST

Example

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BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. The stand-alone executable for blasting two sequences (b12seq) can be retrieved from NCBI ftp site
Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program ☒ blastp ☒ Matrix ☒ Not ApplicableParameters used in BLASTN program only:Reward for a match: Penalty for a mismatch: ☐ Use MegaBLAST Strand option ☒ Both strandsOpen gap 11 and extension gap 1 penalties
gap x_dropoff 50 expect 10.0 word size 3 Filter ☒ AlignSequence 1 Enter accession or GI or download from file Browse
or sequence in FASTA format from: 0 to: 0 LXXXXXXXXLXXEYXXLKEXQALQTVCLSequence 2 Enter accession or GI or download from file Browse
or sequence in FASTA format from: 0 to: 0

B 1/3

VNALRQRVGILEGQLQRLQNAFSQYKK

Align Clear Input

Comments and suggestions to blast-help@ncbi.nlm.nih.gov

B2/3



Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Matrix ☐ BLOSUM62 ☐ gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☒ Align

Sequence 1 lc|seq_1 Length 26

Sequence 2 lc|seq_2 Length 27

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Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", *FEMS Microbiol Lett.* 174:247-250

Program ☒ blastp ☒ Matrix ☐ Not Applicable ☒Parameters used in BLASTN program only:Reward for a match: Penalty for a mismatch: ☐ Use Mega BLAST Strand option ☐ Both strands ☒Open gap and extension gap penalties
gap x_dropoff expect word size Filter ☒ Align Sequence 1 Enter accession or GI or download from file
or sequence in FASTA format from: to Sequence 2 Enter accession or GI or download from file
or sequence in FASTA format from: to

C 1/3

SAALRQOMEALNGKLQRLEAAF SRYKK

Align

Clear Input

Comments and suggestions to blast-help@ncbi.nlm.nih.gov

**Blast 2 Sequences results**

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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Matrix **BLOSUM62** gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☒ Align

Sequence 1 lc|seq_1 Length 26

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Program ☒ blastp ☒ Matrix ☐ Not Applicable ☒

Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch:

☐ Use Mega BLAST Strand option ☐ Both strands ☒

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒ Align

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

LXXXXXXXXXXEVXXLKEXQALQTVCL

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

D 1/3

VNALKQQRVTILDGHLRRFQNAFSQYKK

Align Clear Input

Comments and suggestions to blast-help@ncbi.nlm.nih.gov

D2/3

**Blast 2 Sequences results**

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]Matrix **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0000** wordsize: **3** Filter ☒ Align

Sequence 1 lc|seq_1 Length 26

Sequence 2 lc|seq_2 Length 27

No significant similarity was found

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BLAST 2 sequences

BLAST

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BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using [BLAST](#) engine for local alignment. The stand-alone executable for blasting two sequences (b12seq) can be retrieved from [NCBI ftp site](#)
Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program ☒ blastp ☒ Matrix ☐ Not Applicable ☒Parameters used in [BLASTN](#) program only:Reward for a match: Penalty for a mismatch: ☐ Use [Mega BLAST](#) Strand option ☒ Both strands ☒Open gap and extension gap penaltiesgap x_dropoff expect word size Filter ☒ [Align](#)Sequence 1 Enter accession or GI or download from file [Browse](#)or sequence in FASTA format from: to: LXXXXXXXXXXEVXXLKEXQALQTVCLSequence 2 Enter accession or GI or download from file [Browse](#)or sequence in FASTA format from: to:

E 1/3

VDTLRQRMNLEGEVQRIQNIVTQYRK	
Align	Clear Input

Comments and suggestions to blast-help@ncbi.nlm.nih.gov

**Blast 2 Sequences results**

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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☒ Align

Sequence 1 lc|seq_1 Length 26

Sequence 2 lc|seq_2 Length 27

No significant similarity was found

E 3/3